

REMARKS

The Office has restricted the present application as follows:

Group I, claims 41-46 and 48, drawn to an attenuated *Actinobacillus pleuropneumoniae* bacterium.

Group II, claims 47, 49, and 60, drawn to a method of treating an organism and a method of treating an animal.

Group III, claims 50-52, drawn to an isolated polypeptide, a vector, and a host cell.

Group IV, claims 53, 54, and 56, drawn to a virulent polypeptide encoding by the isolated polypeptide and a composition.

Group V, claim 55, drawn to a method of producing a virulence polypeptide.

Group VI, claim 57, drawn to an antibody.

Group VII, claim 58, drawn to a method of identifying an anti-bacterial agent.

Group VIII, claim 59, drawn to an anti-bacterial agent.

Applicants elect Group I, claims 41-46 and 48, with traverse. As a single disclosed species, Applicants elect SEQ ID NO:51 (corresponding to the gene “DnaJ”).

A group of inventions is considered linked to form a single general inventive concept where there is a technical relationship among the inventions that involves at least one common or corresponding special technical feature. The expression special technical features is defined as meaning those technical features that define the contribution which each claimed invention, considered as a whole, makes over the prior art. M.P.E.P. § 1893.03(d).

Applicants respectfully traverse the restriction requirement between Groups I-VIII. The discrete subset of *A. pleuropneumoniae* genes involved in virulence defines the

special technical feature linking the subject matter of claims 41-60 and is not taught or suggested by the prior art.

The sequences of the pending claims (SEQ ID NOs: 1-56) represent a discrete subset of the A. pleuropneumoniae genome. Applicants selected these particular sequences on the basis of their common and combined role in virulence. This special technical feature is both novel and inventive over the cited prior art documents, which fail to provide any teaching or suggestion of a role for the selected sequences in virulence. For example, the lung lavage methodology cited in document D2 of the International Search Report (Fuller et al., 2000) does not reliably identify any virulence genes (see specification at page 30, lines 3-6; see also Sheehan et al., 2003, page 3962, col. 1, lines 35-39 (cited on the enclosed Form 1449 and attached herewith)). None of the prior art documents identified in the International Search Report, nor cited by the Office, teaches or suggests any selection process that would lead one skilled in the art to the discrete subset of sequences presented in the claims. Applicants submit that the discrete subset of A. pleuropneumoniae genes involved in virulence defines the special technical feature linking the subject matter of the claims 41-60 and is not taught or suggested by the prior art. Withdrawal of the restriction requirement between Groups I-VIII is respectfully requested.

Applicants elect SEQ ID NO:51 (corresponding to the gene "DnaJ") as the species for the purposes of examination. Claims 41-46 and 48 read on the elected species, with claims 41, 42 and 44-46 being generic. Upon the allowance of a generic claim, Applicants are entitled to consideration of claims to additional species which depend from or otherwise require all the limitations of an allowable generic claim. M.P.E.P. § 809.02(a).

Applicants submit that the application is now ready for examination on the merits.
Early notice of such action is respectfully requested.

Respectfully submitted,

A handwritten signature in black ink, appearing to read "Daniel W. Celandier", is written over a horizontal line.

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